CLAIMS

1. An array comprising a plurality of polynucleotide probes immobilized on a solid support, wherein:

(a) the plurality of polynucleotide probes corresponds to a multiplicity of gene transcripts;

(b) each polynucleotide probe of the plurality is localized to a predetermined region on the solid support;

(c) each polynucleotide probe is from about 50 to about 500 nucleotides in length;

(d) each polynucleotide probe is complementary to 3' untranslated sequence of a gene transcript, said untranslated sequence having a defined chromosomal location.

2. An array of claim 1, wherein the plurality of polynucleotide probes comprises at least about 20 polynucleotides, each being complementary to a distinct gene transcript.

3. An array of claim 1, wherein the plurality of polynucleotide probes comprises at least about 100 polynucleotides, each being complementary to a distinct gene transcript.

4. An array of claim 1, wherein the predetermined region comprises at least 2 single-stranded polynucleotides that are complementary to the same gene transcript.

5. An array of claim 1, wherein the predetermined region comprises at least 100 single-stranded polynucleotides that are complementary to the same gene transcript.

6. An array of claim 1, wherein the predetermined region comprises at least 2 single-stranded polynucleotides of identical sequences.

7. An array of claim 1, wherein the predetermined region comprises at least 100 single-stranded polynucleotides of identical sequences.

8. An array of claim 1, wherein the predetermined region has an average size ranging from about 0.01 cm^2 to about 1 cm^2.

9. An array of claim 1, wherein the plurality of polynucleotide probes is immobilized to the solid support via a covalent linkage.

10. An array of claim 1, wherein the solid support is flexible.

11. An array of claim 1, wherein the solid support is rigid.

12. An array of claim 10, wherein the solid support is made of one or more substances selected from the group consisting of nitrocellulose, nylon, polypropylene, glass, and silicon.

13. An array of claim 11, wherein the solid support is made of one or more substances selected from the group consisting of nitrocellulose, nylon, polypropylene, glass, and silicon.

14. An array of claim 1, further comprising a control probe.

15. An array of claim 14, wherein the control probe is selected from the group consisting of normalization control probe, expression level control probe, and mismatch control probe.

16. An array of claim 14, wherein control probe having sequences complementary to one or more constitutively expressed genes.

17. An array of claim 1, where the plurality of polynucleotide probe comprises sequence-tagged site (STS) tages.

18. An array of claim 1, wherein each polynucleotide is amplified using a primer pair selected from the group consisting of SEQ ID NOS. 1-2, 3-4, 5-6, 7-8, 9-10, 11-12, 13-14, 15-16, 17-18, 19-20, 21-22, 23-24, 25-26, 27-28, 29-30, 31-32, 33-34, 35-36, 37-38, 39-40, 41-42, 43-44, 45-46, 47-48, 49-50, 51-52, 53-54, 55-56, 57-58, 59-60, 61-62, 63-64, 65-66, and 67-68.

19. An array of claim 1 further comprising target polynucleotides corresponding to gene transcripts expressed in a subject, wherein the target polynucleotides are bound to the polynucleotide probes in form of stable target-probe complexes.

20. An array of claim 19, wherein the target polynucleotides are conjugated with a detectable label selected from the group consisting of an enzyme, a radioactive and a luminescent substance.

21. An array of claim 19, wherein the target polynucleotides are DNA or RNA molecules.

22. An array of claim 19, wherein the target polynucleotides are cDNAs.

23. A method of preparing an array of polynucleotide probes corresponding to a multiplicity of gene transcripts, said method comprising:

(a) generating a plurality of gene-specific polynucleotides, wherein each polynucleotide of the plurality is from about 50 to about 500 nucleotides in length,

and wherein each polynucleotide is complementary to 3' untranslated sequence of a gene transcript, said untranslated sequence having a defined chromosomal location;

(b) immobilizing the plurality of polynucleotides in a predetermined region on a solid support; and

(c) repeating steps (a) and (b) to yield an array of polynucleotide probes corresponding to a multiplicity of genes.

24. A method of simultaneously detecting expression of a multiplicity of gene transcripts of a subject, comprising:

(a) contacting more than one labeled target polynucleotides corresponding to gene transcripts of said subject with an array of polynucleotide probes of claim 1 under the conditions sufficient to produce stable target-probe complexes; and

(b) detecting the formation of the stable target-probe complexes, thereby detecting expression of a multiplicity of gene transcripts.

25. A method of detecting differential expression of a multiplicity of gene transcripts of at least two subjects, comprising:

(a) contacting more than one labeled target polynucleotides corresponding to gene transcripts of a first subject with an array of polynucleotide probes of claim 1, under the conditions sufficient to produce stable target-probe complexes that form a first hybridization pattern;

(b) contacting more than one labeled target polynucleotides corresponding to gene transcripts of a second subject with an array of polynucleotide probes of claim 1, under the conditions sufficient to produce stable target-probe complexes that form a second hybridization pattern; and

(c) comparing the hybridization patterns, thereby detecting the differential expression of a multiplicity of gene transcripts of the subjects.

26. A method of claim 25, wherein said hybridization patterns are generated on the same array.

27. A method of claim 25, wherein said hybridization patterns are generated on different arrays.

28. A method of claim 25, wherein the target polynucleotides are conjugated with a detectable label selected from the group consisting of an enzyme, a radioactive and a luminescent substance.

29. A method of claim 25, wherein the target polynucleotides are DNA or RNA molecules.

30. A method of claim 25, wherein the target polynucleotides are cDNAs.

31. A method of claim 25, wherein said method further comprises washing said array prior to said detecting step.

32. A kit for simultaneously detecting expression of a multiplicity of gene transcripts comprising an array of claim 1 in suitable packaging.

33. A kit of claim 32, further comprising reagents for generating labeled target polynucleotides corresponding to gene transcripts of a subject.

34. A kit of claim 32, further comprising reagents for hybridization of the target polynucleotides to the polynucleotide probes of the array.

35. A kit for detecting differential expression of a multiplicity of gene transcripts of a test subject in comparison to a control, comprising an array of polynucleotide probes of claim 1 in suitable packaging, wherein the polynucleotide probes is pre-hybridized with polynucleotides corresponding to gene transcripts of the control.

36. A kit of claim 35, further comprising reagents for generating labeled target polynucleotides corresponding to gene transcripts of a subject.

37. A kit of claim 35, further comprising reagents for hybridization of the target polynucleotides to the polynucleotide probes of the array.

38. A computer readable medium having recorded thereon an array of polynucleotide probes of claim 1.

39. A computer readable medium of claim 38, wherein said medium is selected from the group consisting of:

(a) magnetic storage medium;

(b) optical storage medium;

(c) electrical storage medium; and

(d) hybrid storage medium of (a), (b), (c) or (d).

40. A computer readable medium of claim 39, wherein the magnetic storage medium is selected from the group consisting of floppy discs, hard disc, and magnetic tape.

41. A computer readable medium of claim 39, wherein the optical storage medium is CD-ROM.

42. A computer readable medium of claim 39, wherein the electrical storage media is random access memory (RAM) or read only memory (ROM).

43. A computer readable medium of claim 39, wherein the hybrid storage medium is magnetic/optical storage medium.

44. A computer-based system for detecting differential expression of a multiplicity of gene transcripts indicated by a difference in hybridization patterns on an array of polynucleotide probes, comprising:

a) a data storage device comprising a reference hybridization pattern and a test hybridization pattern, wherein the reference hybridization pattern is generated by hybridizing an array of polynucleotide probes of claim 1 with more than one labeled target polynucleotides corresponding to gene transcripts expressed in a control; and wherein the test hybridization pattern is generated by hybridizing an array of polynucleotide probes of claim 1 with more than one labeled target polynucleotides corresponding to gene transcripts expressed in a test subject;

b) search device for comparing the test hybridization pattern to the reference hybridization pattern of the data storage device of step (a) to detect the differences in hybridization patterns; and

c) retrieval device for obtaining said differences in hybridization patterns of step (b).

45. A computer-based system of claim 44, wherein the hybridization patterns are generated on the same array.

46. A computer-based system of claim 44, wherein the hybridization patterns are generated on a different array.

47. A method of determining differential expression of a multiplicity of gene transcripts of at least two subjects using a computer, comprising:

(a) providing a database comprising hybridization patterns that represent expression patterns of multiple genes for a plurality of subjects, wherein each hybridization pattern is generated by hybridizing an array of polynucleotide probes of claim 1 with more than one labeled target polynucleotides corresponding to gene transcripts expressed in a distinct subject, wherein said hybridizing step yields detectable target-probe complexes with different levels of hybridization intensities;

(b) receiving two or more of hybridization patterns for comparison;

(c) determining differences in the selected hybridization patterns; and

(d) displaying the results of said determination.

48. A method of claim 47, wherein the determining step includes the step of calculating differences between the hybridization intensities of target-probe complexes localized in predetermined regions on the solid support.

Added A3